## Sujun Hua

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11490539/publications.pdf

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19	7,290	430874	713466
papers	citations	h-index	g-index
21	21	21	13535
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Epigenetic Activation of WNT5A Drives Glioblastoma Stem Cell Differentiation and Invasive Growth. Cell, 2016, 167, 1281-1295.e18.	28.9	207
2	Targeting YAP-Dependent MDSC Infiltration Impairs Tumor Progression. Cancer Discovery, 2016, 6, 80-95.	9.4	404
3	Telomere Dysfunction Drives Aberrant Hematopoietic Differentiation and Myelodysplastic Syndrome. Cancer Cell, 2015, 27, 644-657.	16.8	85
4	Yap1 Activation Enables Bypass of Oncogenic Kras Addiction in Pancreatic Cancer. Cell, 2014, 158, 185-197.	28.9	553
5	A Comprehensive Nuclear Receptor Network for Breast Cancer Cells. Cell Reports, 2013, 3, 538-551.	6.4	73
6	Glutamine supports pancreatic cancer growth through a KRAS-regulated metabolic pathway. Nature, 2013, 496, 101-105.	27.8	1,562
7	Neutralization of terminal differentiation in gliomagenesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14520-14527.	7.1	65
8	Oncogenic Kras Maintains Pancreatic Tumors through Regulation of Anabolic Glucose Metabolism. Cell, 2012, 149, 656-670.	28.9	1,587
9	Genomic mapping of binding regions for the Ecdysone receptor protein complex. Genome Research, 2009, 19, 1006-1013.	5.5	90
10	Analysis of <i>Drosophila</i> Segmentation Network Identifies a JNK Pathway Factor Overexpressed in Kidney Cancer. Science, 2009, 323, 1218-1222.	12.6	115
11	Genomic Antagonism between Retinoic Acid and Estrogen Signaling in Breast Cancer. Cell, 2009, 137, 1259-1271.	28.9	271
12	BAC TransgeneOmics: a high-throughput method for exploration of protein function in mammals. Nature Methods, 2008, 5, 409-415.	19.0	568
13	Genomic analysis of estrogen cascade reveals histone variant H2A.Z associated with breast cancer progression. Molecular Systems Biology, 2008, 4, 188.	7.2	158
14	Detecting transcriptionally active regions using genomic tiling arrays. Genome Biology, 2006, 7, R59.	9.6	19
15	DBSubLoc: database of protein subcellular localization. Nucleic Acids Research, 2004, 32, 122D-124.	14.5	43
16	A Gene Expression Map for the Euchromatic Genome of Drosophila melanogaster. Science, 2004, 306, 655-660.	12.6	275
17	PSORT-B: improving protein subcellular localization prediction for Gram-negative bacteria. Nucleic Acids Research, 2003, 31, 3613-3617.	14.5	383
18	Proteins with Class $\hat{l}\pm\hat{l}^2$ Fold Have High-level Participation in Fusion Events. Journal of Molecular Biology, 2002, 320, 713-719.	4.2	8

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#	Article	IF	CITATIONS
19	Support vector machine approach for protein subcellular localization prediction. Bioinformatics, 2001, 17, 721-728.	4.1	814